



PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,098

DATE: 01/22/2002

TIME: 13:19:06

Input Set : A:\38053.txt

Output Set: N:\CRF3\01182002\J019098.raw

ENTERED

4 <110> APPLICANT: HAFEN, Ernst
 6 <120> TITLE OF INVENTION: In vivo model system for type-2 diabetes
 8 <130> FILE REFERENCE: 27656/38053
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/019,098
 C--> 11 <141> CURRENT FILING DATE: 2001-12-20
 13 <150> PRIOR APPLICATION NUMBER: PCT/IB99/01166
 14 <151> PRIOR FILING DATE: 1999-06-22
 16 <160> NUMBER OF SEQ ID NOS: 4
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2907
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Drosophila melanogaster
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 30 tactacgata ccgaaaagaa gttcctgcaa agagccgagc caaaaagggt tatatatctg 180
 32 aagaattgct tcaacatcaa tcggcgtttg gacaccaagc atagattttgt catttgctc 240
 34 tctccagag acgggtggatt cgccatcggtt ctcgayaacg aaaaatgatt acgcaaatgg 300
 36 ttggacaaac tactagttct acaaaggaac atagccaatt cgaatggAAC agcgcactca 360
 38 ctttatgacc acgtttggca agttgtcatt caaaaagggtt gtatccggaa gaaagggttggaa 420
 40 atcaccggaa cctaccactg ttgccttact tcaaaatccc tgacattcgt gtgcatttggaa 480
 42 ccggagaaga cgcccaatgg cgaggatcgc gttgcggagca ttgaaataact tttgaccacg 540
 44 atcaggcgat gcggtcatgc atccccacaa tgtatattct acgtggaaact tggccgccaa 600
 46 agtgtcttgg gatctggatg tctgtggatg gajacggata acgcagctat tgctactaat 660
 48 atgcacaaca cgataactgag cgctatgtca gccaaaacag agtgcacac gaatttaata 720
 50 aacgttttac agaatagacc tgacttaagt cacgagccca tgagaaagcg atcgtcgct 780
 52 gcaaacgaag catcgaagcc gataaaacgtaa aatgtcatac aaaatagtca aaactctctc 840
 54 gaatttgcgcgca gctgcagttc gcggccataac tatgggttcg gcagagagag atgcgatagc 900
 56 ttaccaacca gaaatggAAC cctaagcgag tccagcaatc aaacgtactt tggttccaa 960
 58 catggactgc gatccaatac tataatctggc atccgtccgc actcaaccaa caagcatagt 1020
 60 aatagtccaa cgttcaccat gccattaaga tgctcagaat cccaaagatgc atcaattatgt 1080
 62 gtcgatgaat ccgacgacaa cggcagttttt agccactaca gattaaacac gcggcatct 1140
 64 gaaacggcaa ttccgtggaa aacattgtat gactttgcgcgtt gtcggaaattt atttagcaaa 1200
 66 gtcaccgaac aaaatgtaa tgacgaaaac tacataccga tgaatccagt caatcttacc 1260
 68 gatgttatcc atgaaaaggaa gaaggctgat atgcagagat tggaaagatgc ttgcgtcat 1320
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84 gcaaccaatt tggaaaagca gaagttcatc aagaataatg aaattccgaa atacattgaa 1800
 86 aacgtgttcc caaaaagcccc gcgaacggat agctccagcc taactctgca cgccacaagt 1860
 88 caaaaaggaca ttttcaatgg caccaaacta aataacactg cgatcacatc cgaggatgg 1920
 90 tacctcgaga tgaagccagt cggtaatgga tacactccca gttcgaaattt cctgccaatg 1980
 92 aaagtggaga aactcaagct atccgactat cagacagcac cgccactcac cgcaacagcc 2040
 94 gcaccagtgc acgatttaaa caaaaattgc acataacaata tatccgctga gaaatggaga 2100
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 98 agctcgaaac ccacaaatgt cgagagtaca agcaaaagcc atgatgttca ttcagcaa 2220
 100 caaattgatt gcgagaaaatgt gtgcgcgcag agcagcgcata agctaaataa tcatctggcc 2280
 102 gacaagatttgcgagaacaa caatttggat ataggcgggc atgaggaaaa gaagtgggtt 2340
 104 cattcgataa gcagcgaaga ctacacacaa atcaaggaca aatcgaatga tttcacaaaa 2400
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 110 agtgtgaata cgattcccgta taatgccacc gccaccgcgg tgagcagcag ctcactcacc 2580
 112 aaattcaata taaattcgcgaa aagccagcc gcccgcgcg attcgcgtac cactggcaca 2640
 114 gatccaagta caccacagaa cattctacag attaaagatt tgaatttccc ctcaaggtcg 2700
 116 tcgtctcgca tatcccagcc ggagctgcac taccccgcc tagatctcc ccattgcagt 2760
 118 ggccaaaatc cagctaaata cctgaagaga ggatcacgcg aatcgccccc ggtgtccgca 2820
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 130 <211> LENGTH: 2907
 131 <212> TYPE: DNA
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 134 <220> FEATURE:
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 136 <222> LOCATION: (1)..(2907)
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 141 1 5 10 15
 143 aag ctg aag acc atg aag aag aag ttc ttt gtg ctg tac gag gag acg 96
 144 Lys Leu Lys Thr Met Lys Lys Phe Phe Val Leu Tyr Glu Glu Thr
 145 20 25 30
 147 agc act tcg gca gcc cgg ctg gag tac tac gat acc gaa aag aag ttc 144
 148 Ser Thr Ser Ala Ala Arg Leu Glu Tyr Tyr Asp Thr Glu Lys Phe
 149 35 40 45
 151 ctg caa aga gcc gag cca aaa agg gtt ata tat ctg aag aat tgc ttc 192
 152 Leu Gln Arg Ala Glu Pro Lys Arg Val Ile Tyr Leu Lys Asn Cys Phe
 153 50 55 60
 155 aac atc aat cgc cgt ttg gac acc aag cat aga ttt gtc att gtg ctc 240
 156 Asn Ile Asn Arg Arg Leu Asp Thr Lys His Arg Phe Val Ile Val Leu
 157 65 70 75 80
 159 tcc tcc aga gac ggt gga ttc ggc atc gtt ctc gag aac gaa aat gat 288
 160 Ser Ser Arg Asp Gly Gly Ile Val Leu Glu Asn Glu Asn Asp
 161 85 90 95
 163 tta cgc aaa tgg ttg gac aaa cta cta gtt cta caa agg aac ata gcc 336
 164 Leu Arg Lys Trp Leu Asp Lys Leu Val Leu Gln Arg Asn Ile Ala
 165 100 105 110

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167 aat tcg aat gga aca gca cac tca cct tat gac cac gtt tgg caa gtt	384
168 Asn Ser Asn Gly Thr Ala His Ser Pro Tyr Asp His Val Trp Gln Val	
169 115 120 125	
171 gtc att caa aag aag ggt att tgc gag aaa gtt gga atc acc gga acc	432
172 Val Ile Gln Lys Lys Gly Ile Ser Glu Lys Val Gly Ile Thr Gly Thr	
173 130 135 140	
175 tac cac tgt tgc ctt act tca aaa tcc ctg aca ttc gtg tgc att gga	480
176 Tyr His Cys Cys Leu Thr Ser Lys Ser Leu Thr Phe Val Cys Ile Gly	
177 145 150 155 160	
179 ccg gag aag acg ccc aat ggc gag gat cgc gtt gcg agc att gaa ata	528
180 Pro Glu Lys Thr Pro Asn Gly Glu Asp Arg Val Ala Ser Ile Glu Ile	
181 165 170 175	
183 ctt ttg acc acg atc agg cga tgc ggt cat gca tcc cca caa tgt ata	576
184 Leu Leu Thr Thr Ile Arg Arg Cys Gly His Ala Ser Pro Gln Cys Ile	
185 180 185 190	
187 ttc tac gtg gaa ctt ggc cgc caa agt gtc ttg gga tct ggt gat ctg	624
188 Phe Tyr Val Glu Leu Gly Arg Gln Ser Val Leu Gly Ser Gly Asp Leu	
189 195 200 205	
192 tgg atg gag acg gat aac gca gct att gct act aat atg cac aac acg	672
193 Trp Met Glu Thr Asp Asn Ala Ala Ile Ala Thr Asn Met His Asn Thr	
194 210 215 220	
196 ata ctg agc gct atg tca gcc aaa aca gag tcg aac acg aat tta ata	720
197 Ile Leu Ser Ala Met Ser Ala Lys Thr Glu Ser Asn Thr Asn Leu Ile	
198 225 230 235 240	
200 aac gtt tat cag aat aga cct gac tta agt cac gag ccc atg aga aag	768
201 Asn Val Tyr Gln Asn Arg Pro Asp Leu Ser His Glu Pro Met Arg Lys	
202 245 250 255	
204 cga tcg tcg tct gca aac gaa gca tcg aag ccg ata aac gta aat gtc	816
205 Arg Ser Ser Ala Asn Glu Ala Ser Lys Pro Ile Asn Val Asn Val	
206 260 265 270	
208 ata caa aat agt caa aac tct ctc gaa ttg cgc agc tgc agt tcg ccc	864
209 Ile Gln Asn Ser Gln Asn Ser Leu Glu Leu Arg Ser Cys Ser Ser Pro	
210 275 280 285	
212 cat aac tat ggt ttc ggc aga gag aga tgc gat agc tta cca acc aga	912
213 His Asn Tyr Gly Phe Gly Arg Glu Arg Cys Asp Ser Leu Pro Thr Arg	
214 290 295 300	
216 aat gga acc cta agc gag tcc agc aat caa acg tac ttt ggt tcc aac	960
217 Asn Gly Thr Leu Ser Glu Ser Ser Asn Gln Thr Tyr Phe Gly Ser Asn	
218 305 310 315 320	
220 cat gga ctg cga tcc aat act ata tct ggc atc cgt ccg cac tca acc	1008
221 His Gly Leu Arg Ser Asn Thr Ile Ser Gly Ile Arg Pro His Ser Thr	
222 325 330 335	
224 aac aag cat agt aat agt cca acg ttc acc atg cca tta aga tgc tca	1056
225 Asn Lys His Ser Asn Ser Pro Thr Phe Thr Met Pro Leu Arg Cys Ser	
226 340 345 350	
228 gaa tcc gaa gag tca tca att agt gtc gat gaa tcc gac gac aac ggc	1104
229 Glu Ser Glu Glu Ser Ser Ile Ser Val Asp Glu Ser Asp Asp Asn Gly	
230 355 360 365	
232 agt ttt agc cac tac aga tta aac acg cgg tca tct gag acg gca att	1152

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234 370 375 380			
236 cct gag gaa aac att gat gac ttt gcc agt gcg gaa tta ttt agc aaa	1200		
237 Pro Glu Glu Asn Ile Asp Asp Phe Ala Ser Ala Glu Leu Phe Ser Lys			
238 385 390 395 400			
240 gtc acc gaa caa aat gta agt gac gaa aac tac ata ccg atg aat cca	1248		
241 Val Thr Glu Gln Asn Val Ser Asp Glu Asn Tyr Ile Pro Met Asn Pro			
242 405 410 415			
244 gtc aat cct acc gat gct atc cat gaa aag gag aag gct gat atg cag	1296		
245 Val Asn Pro Thr Asp Ala Ile His Glu Lys Glu Lys Ala Asp Met Gln			
246 420 425 430			
248 aga ttg gaa gat gct tcg ctg cat ttc aac ttt ccg gag cac gcg tcg	1344		
249 Arg Leu Glu Asp Ala Ser Leu His Phe Asn Phe Pro Glu His Ala Ser			
250 435 440 445			
252 gaa aag ctt gct aag gat ttt gat ctg gac tct gat aac caa tgc tgt	1392		
253 Glu Lys Leu Ala Lys Asp Phe Asp Leu Asp Ser Asp Asn Gln Cys Cys			
254 450 455 460			
256 cgt ccc att cgc gcc tat tcg ata ggc aac aag gtt gag cat tta aag	1440		
257 Arg Pro Ile Arg Ala Tyr Ser Ile Gly Asn Lys Val Glu His Leu Lys			
258 465 470 475 480			
260 ttt aat aag cgc ctg gga cac ttg aat gat acg gga cag aat ccg aat	1488		
261 Phe Asn Lys Arg Leu Gly His Leu Asn Asp Thr Gly Gln Asn Pro Asn			
262 485 490 495			
264 cgc gtg cga gcc tac tcg gtt ggc tcc aaa tcg aag ata ccg cgc tgc	1536		
265 Arg Val Arg Ala Tyr Ser Val Gly Ser Lys Ser Lys Ile Pro Arg Cys			
266 500 505 510			
268 gac ctg cag cga gtg gtc ctc gtg gag gac aat aaa cat gag ttc aca	1584		
269 Asp Leu Gln Arg Val Val Leu Val Glu Asp Asn Lys His Glu Phe Thr			
270 515 520 525			
272 gcg aat agg agt cag agt agc att acc aag gaa gga acc agc tat ggc	1632		
273 Ala Asn Arg Ser Gln Ser Ser Ile Thr Lys Glu Gly Thr Ser Tyr Gly			
274 530 535 540			
276 agc agt gcc aat cga caa aag aac tcc aca agt gct cca ctc ctc agt	1680		
277 Ser Ser Ala Asn Arg Gln Lys Lys Ser Thr Ser Ala Pro Leu Leu Ser			
278 545 550 555 560			
280 ctg aag aac cag ata aac tcc gac cga atg agt gac tta atg gaa att	1728		
281 Leu Lys Asn Gln Ile Asn Ser Asp Arg Met Ser Asp Leu Met Glu Ile			
282 565 570 575			
284 gat ttt tca caa gca acc aat ttg gaa aag cag aag ttc atc aag aat	1776		
285 Asp Phe Ser Gln Ala Thr Asn Leu Glu Lys Gln Lys Phe Ile Lys Asn			
286 580 585 590			
288 aat gaa att ccg aaa tac att gaa aac gtg ttc cca aaa gcc ccg cga	1824		
289 Asn Glu Ile Pro Lys Tyr Ile Glu Asn Val Phe Pro Lys Ala Pro Arg			
290 595 600 605			
292 acg gat agc tcc agc cta act ctg cac gcc aca agt caa aag gac att	1872		
293 Thr Asp Ser Ser Leu Thr Leu His Ala Thr Ser Gln Lys Asp Ile			
294 610 615 620			
296 ttc aat ggc acc aaa cta aat aac act gcg atc aca tcc gag gat ggt	1920		
297 Phe Asn Gly Thr Lys Leu Asn Asn Thr Ala Ile Thr Ser Glu Asp Gly			

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302																	655
304																	2016
305	cgc	ctg	cca	atg	aaa	gtg	gag	aaa	ctc	aag	cta	tcc	gac	tat	cag	aca	
306	Cys	Leu	Pro	Met	Lys	Val	Glu	Lys	Leu	Lys	Leu	Ser	Asp	Tyr	Gln	Thr	
308																	2064
309	gca	ccg	cca	ctc	acc	gca	aca	gcc	gca	cca	gtg	cac	gat	tta	aac	aaa	
310	Ala	Pro	Pro	Leu	Thr	Ala	Thr	Ala	Ala	Pro	Val	His	Asp	Leu	Asn	Lys	
312																	2112
313	675																
314	Ile	Ser	Thr	Tyr	Asn	Ile	Ser	Ala	Glu	Lys	Trp	Arg	Glu	Gln	Pro	Ser	
316																	2160
317	aga	agc	gag	gaa	aag	tcg	aac	tcg	cca	ttg	aat	gac	aac	acc	ttt		
318	Arg	Ser	Glu	Glu	Lys	Lys	Ser	Asn	Ser	Pro	Leu	Asn	Asp	Asn	Thr	Phe	
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320	705																2208
321	Ser	Ser	Lys	Pro	Thr	Asn	Val	Glu	Ser	Thr	Ser	Lys	Ser	His	Asp	Val	
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324	725																2256
325	cat	tca	gca	aat	caa	att	gat	tgc	gag	aaa	gtg	tgc	gcg	cag	agc	agc	
326	His	Ser	Ala	Asn	Gln	Ile	Asp	Cys	Glu	Lys	Val	Cys	Ala	Gln	Ser	Ser	
328																	750
329	740																2304
330	Asp	Lys	Leu	Asn	Asn	His	Leu	Ala	Asp	Lys	Ile	Val	Glu	Asn	Asn	Asn	
331																	765
332	755																2352
333	ttg	gat	ata	ggc	ggg	cat	gag	gaa	aag	ttg	gtt	cat	tcg	ata	agc		
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336																	780
337	770																2400
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339																	795
340	785																800
341	ttt	aac	gaa	gcc	ggc	tac	aaa	att	ctg	caa	att	aaa	agc	gac	agc	tca	
342	Phe	Asn	Glu	Ala	Gly	Tyr	Lys	Ile	Leu	Gln	Ile	Lys	Ser	Asp	Ser	Ser	
344																	815
345	805																2448
346	ctc	atc	tca	tgc	aag	cta	tac	caa	aag	gtt	ata	cac	aag	gat	aac	ttg	
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348																	2496
349	820																830
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353	835																840
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356																	2592
357	850																845
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361																	2688
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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date